AMENDMENTS TO THE SPECIFICATION:

Please amend paragraph [0018] on page 12 of the specification as follows:

Further, in the detection method of the present invention, a nucleic acid sample is prepared from a dog, and a base corresponding to a base at position 1117 of a canine CYP1A2 gene (i.e., at position 87 of exon 4) is determined, to detect or determine which dog is an extensive metabolizer (EM) or a poor metabolizer (PM) in the rate of drug metabolism. When the base is a C/C genotype or a C/T genotype, it can be judged that the dog is EM. When the base is a T/T genotype, it can be judged that the dog is PM. As the ~~PM~~ EM, the C/C genotype is preferable.